Analysis of SIR Mathematical Model for Malaria Disease: A Study in Assam, India

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ABSTRACT

The global outbreak of covid-19 pandemic is still affecting people around the globe very badly. Before the covid-19 pandemic outbreak, several research works were done for the detection and prevention of various infectious diseases using different mathematical modeling. Implementing mathematical modeling to resolve problems in Biology and physiology is generally called Mathematical Biology, an extremely interdisciplinary area. The applications of mathematical modeling in the analysis of infectious diseases help to concentrate on the necessary processes associated with forming the infectious disease epidemiology and specifications estimation. The compartmental mathematical model can be either SI, SIS, SIR, SIRS, or SEIR where S, I, R, and E denote susceptible, infected, recovered, and exposed respectively. Malaria is an infectious disease that has a large economic and health impact on society. This study aims to predict the estimation of suspected, infected and recovered people using the SIR mathematical model of the Barama area of Baksa District in Assam, India. Here we analyzed the Basic Reproductive Ratio of the SIR model for malaria disease and examined if malaria is epidemic or endemic in that area.

Keywords: Mathematical biology, epidemiology, mathematical model, SIR model.

INTRODUCTION

Mathematical Biology is a multidisciplinary area. It is a branch of biology that uses mathematical models for the analysis and representation of living organisms. It includes mathematical sciences including statistics, operational research, and scientific computing. The main purpose of mathematical biology is to model natural biological processes using mathematical techniques and tools. Mathematical epidemiology is one of the oldest and richest areas of mathematical biology.

Epidemiology is an area of science that is involved in the investigation of the sources, spreading, and disease dominance. It has remarkably strengthened our perception of how pathogens appear, develop, and grow. The relationship between mathematics and epidemiology is gaining popularity. For mathematicians, epidemiology brings thrilling areas and for the epidemiologist, mathematical modeling provides key research tools for disease occurrence. Over the last few years, mathematical modeling has turned into a fascinating tool for understanding infectious disease epidemiology and dynamics. In the analysis of infectious diseases, mathematical modeling has been utilized for more than a century. Epidemic modeling provides a perception of disease spread, disease form, and their pathogen-related (e.g., age) determinants. They allow us to evaluate key parameters, emphasize crucial gaps in data, develop new hypotheses and forecast population-level effectiveness.

Lack of understanding of infectious disease dynamics is not only a matter of concern in the field of academic pursuit but is still a threat to mankind. The bubonic plague outbreak appeared in China in late 1320. The bacteria Yersinia has created the disease and it spreads to people from rats through fleas. The epidemic had started to spread in West China. In Europe, the first major outbreak occurred in 1347. After that, the black death appeared, and many people lost their lives due to that disease. Throughout the year 1918-1919, about 100 million people lost their lives worldwide due to Influenza or Spanish flu pandemics.

Figure 1. Approximate death of people due to COVID -19 Pandemic (Source: Google)

The AIDS epidemic, which has its origin in Africa, was first recognized in 1981 in the USA. Almost 25 million people had lost their lives due to this disease at that time. In the world, a child dies every 2 minutes due to malaria (WHO). Malaria is a mosquito-borne parasitic infection spread by a female Anopheles mosquito infected by the Plasmodium parasite. It is a single-celled parasite that multiplies amongst the red blood cells of humans as well as in the mosquito's intestine. When the female mosquito feeds on an infected person, the parasites are ingested along with the human blood. The parasites multiply in the mosquito's gut and these infectious forms are passed onto another human when the mosquito feeds again. The symptoms of the disease may occur within 1 or 3 weeks after being infected. There are four species of the Plasmodium parasite that can infect the female Anopheles mosquito and cause malaria in humans- Plasmodium falciparum, Plasmodium Ivax, Plasmodium vale, and Plasmodium malariae. Some of the symptoms of malaria patients are abdominal pain, chills and sweat, high fever, headache, etc. Since no effective vaccine has developed to date and many of the older anti-malarial drugs are losing effectiveness due to the parasite evolving drug resistance, prevention (using bed nets) is still the only advisory given to the affected person.

The first researcher who experimented with the mathematical model for infectious disease in a population was Daniel Bernoulli, who had discussed the consequences of variolation of smallpox disease in 1766 in his research article. He found that universal inoculation against smallpox would grow the life span to 29 years 9 months from 26 years 7 months (Karjai et al., 2020). (Alexander, 2004) recommended some popular approaches to examine the dynamic nature of epidemiological systems and the bifurcation techniques they go through at their different equilibrium points. One practical analytical tool is numerical simulations. Shikha (Singh et al., 2005) studied the effects of migrations of people for the increasing number of malaria cases and they proposed and analyzed SIS and SIRS epidemic models. Sangeeta (Venkatachalam et al., 2006) put forward a global stochastic field simulation paradigm (GSFS) for the modeling and simulation of infectious disease epidemics. (Johnson et al., 2009) analyzed the mathematical modeling of infectious disease using the SIR model. (Imane et al., 2014) studied the SIR model to describe epidemic modeling. (Daughton et al., 2017) observed the lack of cooperation amongst the public health policy group and the modeling community for a decrease of infectious disease spread. (Karsai et al., 2020) tried to explain the ongoing transmission dynamics of varicella-zoster virus (VZV) in Hungary. They calculated some important disease variables. (Sweileh, 2022) discusses comprehensive research act on the prevention and control of infectious disease outbreaks through epidemic modeling. From the review of the literature, it is clear that very few works on SIR modeling on infectious disease outbreaks in India have been reported till now. Again, based on the literature review, it is found that epidemic modeling and simulation is one of the growing and emerging new areas of research.

The state of Assam (India) is combating some major problems like floods, landslides, and erosion. To make matters worse, it is also combating some major infectious diseases like Japanese Encephalitis (JE), Dengue, Malaria, Chikungunya, Chickenpox, etc. Thus, infectious diseases put the healthcare infrastructure of the state under severe pressure. Again, the epidemiology of malaria and other diseases are not deliberately observed and the affected area of Barama, Assam, India signifies that a large portion of people get affected.

Our work mainly focuses on studying the infectious disease Malaria in the Alagjar area of Baksa District of Assam, India by developing an epidemiological model (SIR model) and to have an insight into the spread of malaria in those localities. The SIR model is studied and applied in different areas all over the world but there is a need for a modified SIR model for accurate estimation of infectious diseases concerning case studies. Motivated by this, which is not yet sufficient, our research also aims to clearly understand Mathematical Biology and by developing an epidemiological model for infectious disease malaria. Prevention and control measures can be adopted which have significant public health importance. Specifically, there is a need for such a kind of mathematical modeling and analysis for rapid disease diagnostics.

METHODOLOGY

Here, to describe the epidemiology, the SIR (Susceptible-Infected-Recovered) model is applied. This model was first proposed in 1927 by Kermack and McKendrick and it is one of the famous epidemic models to study the spreading of infectious diseases.

In the SIR model, there are three compartments based on disease spread. They are suspected people (S), infected people (I), and recovered people (R). Once a person has recovered, they become immune and they are not susceptible, nor infected anymore.

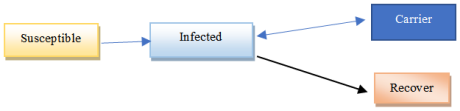

Figure 2. SIR Model in Epidemiology

An epidemic appears in a population if a very minute number of people get infected in a susceptible group developing more numbers of infected people. The severity of the diseases can be studied through the SIR epidemic model. This model establishes the fact that there lives a threshold frequency of susceptibility, and it should be exceeded for an infection to occur and for the outbreak of diseases.

Purposeful data collection and proper analysis of data are vital components of epidemiology. These data are accomplished to identify trends, can build general predictions, and can evaluate the limitations of those predictions. Such predictions can be immensely inaccurate unless extracted mathematically and here lies the use of mathematical modeling. The present work has been executed by utilizing primary data on infectious disease, viz. malaria collected from the district health center, Barama, Baksa, Assam, India. The line listing of malaria data was acquired from Barama BPHC, Baksa, Assam, India from January to March 2017.

The equations of the model are resolved arithmetically with MATLAB and Origin Lab software. Simulations are carried out on the model equations to resolve the consequences of the values on disease spread.

Let us assume that there are three types of people in that group designated by suspected (S), infected (I), and recovered (R). All these are functions of time (t). It can be altered by some differential equations.

The assumptions to evolve this SIR model are as follows:

1) The total number of people is stable in that locality.
2) If a person gets infected, he or she will leave the suspected compartments. If the person gets well then, he or she will leave the infected compartments and will earn resistance to the disease.
3) The probability of being infected with the disease does not depend on factors like age, sex, social status, or race.
4) There is no inherited immunity in the people.
5) The people are mixed homogeneously.

The model starts with the following notations:

$S(t)$ is the number of suspected people at time t ,
$I(t)$ is the number of infected people at time t ,
$R(t)$ is the number of removed people at time t,
and N is the entire population.

The assumptions guide to a set of differential equations:

$$dS/\,dt \;=\; -\beta S(t)\, I(t) \quad (1)$$
$$dI/dt = (\beta S(t) - K) I(t) \quad (2)$$
$$dR/dt \;= KI(t) \quad (3)$$

Here K denotes the recovery rates, β is the average amount of communication in a given period from an infectious people.

When the total number of populations is N, then.

$$N = S(t) \;+\; I(t) \;+\; R(t) \quad (4)$$

After using Euler's method of systems, the differential equations can be determined. Thus,

$$S_{n+1} \;=\; S_n - \beta\, S_n\, I_n \quad (5)$$
$$I_{n+1} \;=\; I_n\, (1 + \beta S_n - K)\Delta t \quad (6)$$
$$R_{n+1} \;=\; R_n \;+\; K\, I_n\, \Delta t \quad (7)$$

where, S_{n+1} , I_{n+1} and R_{n+1} denoted the amount of suspected, infectious and removed individuals at time $(n+1)$.

The Basic Reproductive Ratio (B_R), is one of the prime factors of epidemic modeling. It can predict if the population is in a dangerous state or not. The secondary individuals likely to be infected by an individual throughout the person's whole period of infection can be called Basic Reproductive Ratio. The computation and understanding of the value of the Basic Reproductive Ratio performs a pivotal part in gaining knowledge about the outbreak and probable risk from impending infectious disease. If the value of the Basic Reproductive Ratio is analyzed either because of its numerical value or region of the infectiousness curve, then it supports the evaluation of the comparative essential transmissibility of pathogens.

B_R is influenced by the transmission rates and recovery rates, i.e., β *and* K.

It is achieved by

$$B_R \;= \beta \;/\; K$$

The Basic Reproductive Ratio is obtained by the as-developed SIR model with the help of MATLAB programming where the time-dependent transmission rate (β), which is calculated using the suspected, infected and recovered population for the particular time period (1- 10 days) is the model input. β is calculated incorporating the susceptible in n days and in $n+1$ days, and infectious in n days where $n =$ 0,1,2,3 .... are the input parameters. The number of suspected, infected and recovered population in Alagjar area for all the 10 days collected from the Barama BPHC (as given in Table1), are the input used to calculate β. For all the ten days (from day 1 to day10), β is calculated which is nonlinear as shown in figure 4. The as-obtained time-dependent β is used as model input to estimate the B_R. The rate of recovery rate (K) which varies from 0.01 to 1.00 (such as which is 0.66 in day 8) is another time-dependent model input used to obtain the value of B_R.

Hence, ratio of the time-dependent β and K gives the B_R as shown in Figure 5. Thus, the B_R is a dynamic factor on which the disease outbreak depends.

If the value of the Basic Reproductive Ratio is greater than 1, then the incidence of disease will grow. On the other hand, if the value of B_R is less than 1, the incidence of disease will be reduced, and the disease will die out. If $B_R = 1$, then the incidence of disease will be stable.

For vector-borne diseases like dengue, the basic reproductive ratio value is computed from the survival function.

RESULTS AND DISCUSSION

An experimental survey was taken for the Alagjar sub-center under Barama BPHC in Baksa Assam, India where a population up to 4937 people is living homogeneously and the modeling for malaria disease has been done using the SIR model.

Figure 3 shows the number of infected people in Barama BHPC in Assam between the years 2009 to 2016. It can be clearly seen that the number of positive Malaria cases was dramatically increases in 2010 and then gradually decreases. From 2009 to 2015, 945 cases of malaria were reported in Barama B.P.H.C. under Baksa district, with a minimum incidence rate of 4.87% per 10,000(total population 75884) in 2015 and maximum incidence rate 28.3% (total population 79646) in the year 2010. In 2009, the incidence rate was 27.06%. During 2009-15, in 2010 larger increase of incidence rate is there in comparison to all the other years and it was gradually decreases from 2011 -2015. In 2016, there is an increase in the number of positive cases again in the same epidemic area which motivated to consider the year 2016 in the present study.

Again, it is to be mentioned here that Sub-Centre Wise Epidemiological Report 2016, Barama BPHC has been collected in which there is having 18 sub-centers. Among the 18 sub-centers, in Alagjar subcenter during the malaria outbreak in the year 2016, the number of positive cases is maximum (10 numbers) though the population (4937) is not maximum (maximum population of Barama PHC is 13020 but +ve cases is 8), which encourages to consider the Alagjar sub-center for the SIR modeling. Figure 4 shows the rate of suspected, infected, and recovered people in that time.

When the number of days of disease spreads gets older, the recovery rate increases. The number of suspected persons decreases with time and the infected person's rate is almost constant during the whole time.

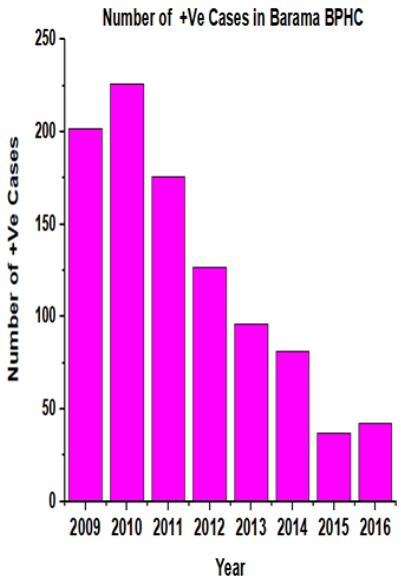

Figure 3. Total Number of +Ve cases for Barama BPHC from the year 2009 - 2016.

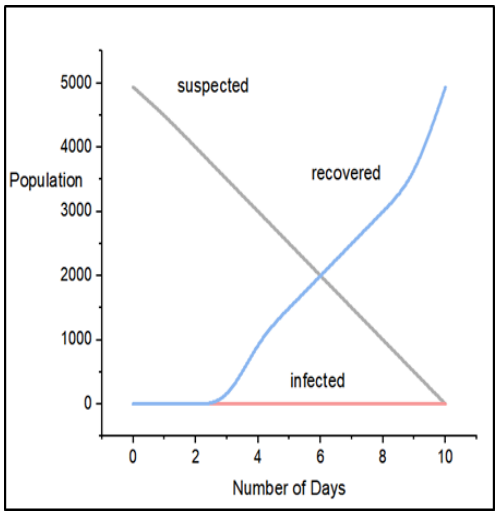

Figure 4. The effect of malaria in the Alagjar area of Assam, India.

Table 1 shows the observed recovery rate from the first day to the last 10th day of the disease outbreak. S, I, R is time-dependent and at the beginning of the epidemic, total population is considered as suspected since the vaccination status is not known. But the model input parameter for the present model are variables, as the number of suspected and infected people is not fixed for the whole study as shown in the table, which makes this model more accurate.

Table 1. Observed Rate of Recovery

Period	S (Suspected)	I (Infected)	R (Recovered)
0	4937	0	0
1	4500	1	0
2	4000	0	0
3	3500	3	0
4	3000	2	1000
5	2500	0	1500
6	2000	2	2000
7	1500	1	2500
8	1000	1	3000
9	500	0	3500
10	0	0	4937

For the Alagjar sub center under Barama BPHC in Assam, India, throughout the outbreak period, the transmission rate is estimated by the present SIR model and is shown in Figure 5. It shows the rate of transmission and Figure 6 shows the Basic Reproductive Ratio for that time. Poisson, Geometric, and Binomial distribution could be shaped when contact tracing is present which gives adequate data for the establishment of actual offspring distribution during several contemporary epidemics. When an outbreak occurs and the transmission rate and the amount of suspected people expected to encounter the pathogen, then the rate of transmission is measured. It permits sources to be fixed in such a manner that an outbreak can hold in under a tiny amount of time and the amount of contact decreases. In the evolution of an outbreak in terms of rate of spread and the numbers of susceptible individuals likely to encounter the pathogen, rate of transmission is the measure. This allows resources to be focused on such a way that an outbreak can be contained within the shortest period and the number of contacts is minimized.

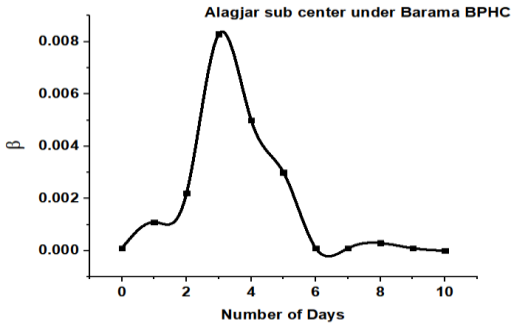

Figure 5: The rate of transmission vs. time period for malaria disease in Alagjar area, Barama, Assam, India.

From the present modeling for the outbreak of Malaria disease in Alagjar area, Barama, Assam, India, it is observed that the rate of transmission (β) from day 3 to day 5 is high, and on the 5th day, the rate of transmission $\beta = 0.008$ which is maximum(as shown in figure5).

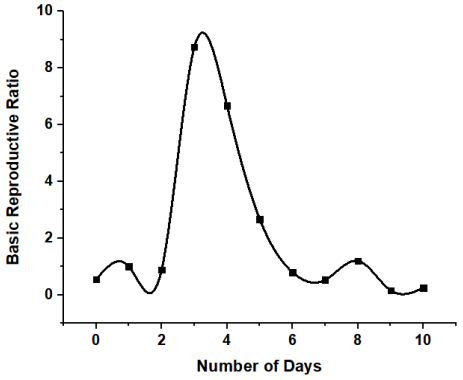

Figure 6: Basic Reproductive Ratio vs. time period for malaria disease in Alagjar area, Barama, Assam, India.

From the present modeling, it is observed that from day 3 to day 8, the basic reproductive ratio B_R>1 and as a result the disease incidence will grow. As shown in figure 6, on day 3, $B_R = 8.74$, which is maximum and thus the indication of peak time of spreading the malaria in the area. In day 1, and the last 2 days (9th and 10th) when B_R <1, the infected number is negligible and in the last three days, number of recovered is more in comparison to the suspected, which agrees very well with the actual data as collected. When $B_R = 1$, the incidence of disease will be stable. In the present study also, as found from the experimental result the rate of infection on day 1 and day 8 is the same ($B_R = 1$), which agrees with the results obtained from the present model. In day 9 and day 10, as the suspected is significantly decrease along with the increase in recovery, thus the value of B_R is very less, resulting non recurrence of disease outbreak and switching to normal condition. On day 9, $B_R = 0.16$ and on day 10, $B_R = 0.25$. From the data collected from the Public Health Centre of Barama, on day 9, the suspected population is 500, with infected person 0 and on day 10, both suspected and infected population is 0. As a result, the basic reproductive ratio is very very less than 1,which justifies the accuracy of the present model for estimation of malaria disease outbreak incorporating time-dependent model parameter.

CONCLUSION

We have formulated and analyzed the SIR model for malaria disease outbreak in the year 2016 in Alagjar Sub Centre in Baksa district, Assam, India for a period of 10 days. The Basic Reproductive Ratio is obtained from the as-developed SIR model incorporating time-dependent transmission rate and recovery rate as model input. From the data, we have found that the value of Basic Reproductive Ratio is less than 1 during the 9th & 10th days of the disease spreading, which indicates that the disease is under control.

REFERENCES

Alexander ME. 2004. Mathematical Modeling of Infectious Diseases: Methods and Some Results. *IEEE Annual Meeting of Fuzzy Information, 2004. Processing NAFIPS '04*. **2**: 675-679.

Affandi, Pardi & Faisal. 2018. Optimal Control Mathematical SIR Model of Malaria Spread in South Kalimantan. *Journal of Physics: Conf. Ser*. **1116**(2): 1-17.

Daughton A. *et al*. 2017.An approach to and web-based tool for infectious disease outbreak intervention analysis. *Sci Rep*. **7**: 46076.

Devi R & Choudhury BKD. 2018. SIR Model-based Study on Chicken Pox Outbreak in Kamrup (M) District of Assam, India. *International Journal of Computer Applications*. **182(**20): 1-4.

Devi R & Choudhury BKD. 2020. Mathematical Modelling of Infectious Diseases with Special reference to Malaria Disease. *Journal of the Social Sciences.* **48**(3): 2408-2417.

Imane BEL *et al*. 2014. Stochastic Study for SIR Model. *Applied Mathematical Sciences*. **8**: 405-413.

Jonshon T. 2009. *Mathematical Modeling of Diseases: Susceptible-Infected-Recovered (SIR) Model*. University of Minnesota, Morris. http://www.morris.umn.edu/academic/math/Ma4901/Sp09/Final/TeriJohnson-Final.pdf.

Karsai J. *et al*. 2020. Modeling the transmission dynamics of varicella in Hungary. *Journal of Mathematics in Industry.* **10**: 12.

Kretzschmar M & Wallinga J. 2009. *Modern Infectious Disease Epidemiology*. New York: Springer.

Pandiyan M & Sindhu DS. 2022. Fuzzy SIR-Epidemic Model for Transmission of Malaria. *ECS Transactions*. **107**: 7691

Schneeweiss S. 2006. Sensitivity Analysis and External Adjustment for Unmeasured Confounders in Epidemiologic Database Studies of Therapeutics. *Pharmacoepidemiology and Drug Safety*. **15(**5): 291-303.

Singh S. *et al*. 2005. Modelling and Analysis of The Spread of Malaria: Environmental and Ecological Effects. *Journal of Biological Systems*. **13(**01): 1-12.

Smith NR. *et al*. 2018. Agent-based Models of Malaria Transmission: A Systematic Review. *Malaria Journal*. **17**(1): 299.

Sweileh WM. 2022. Global Research Activity on Mathematical Modeling of Transmission And Control of 23 Selected Infectious Disease Outbreak. *Globalization and Health*. **18**(4).

Venkatachalam S & Mikler AR. 2006. Modeling infectious diseases using global stochastic field simulation**.** *2006 IEEE International Conference on Granular Computing*. Atlanta: IEEE.

Wedajo AJ. et. al. 2018. Analysis of SIR Mathematical Model for Malaria Disease With The Inclusion of Infected Immigrants. *IOSR Journal of Mathematics.* **14**: 10-21.

Kumar D. *et al.* 2019. A New Fractional SIRS-SI Malaria Disease Model With Application of Vaccines, Antimalarial Drugs, and Spraying. *Adv Differ Equ*. **278(**2019).

Badshah N & Akbar H. 2021. Stability Analysis of Fractional Order SEIR Model for Malaria Disease in Khyber Pakhtunkhwa. *Demonstratio Mathematica*. **54**(1): 326-334.

Oke IS. *et al*. 2020. Mathematical Modeling of Malaria Disease with Control Strategy.Commun. Math. Biol. *Neurosci*. **2020**: 43.

Ibrahim MM. *et al*. 2020. Impact of Awareness to Control Malaria Disease: A Mathematical Modeling Approach. *Complexity*. **2020:** 8657410.